

Ex 12
 6 AGA GGG AATTCGGCACGAGGCAGCATGGAGCCTTCGGCTGACTGGCTGGCC
 GA GAA CAG
 NT 16.20.1
 Ex 1
 24
 ACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTG
 Ex 13
 NT 16.3
 GAGGCGGTGGCGCTGCCCAACGCACCGAATAGTTACGGTCGGAG
 J(2) J(1)
 Ex 14
 GCCGATCAGGTCATGATGATGGGCAGCGCCCCGAGTGGCGGAG
 Ex 2
 Ex 2
 CTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCA
 16 INT
 CTCTACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCTGGAC
 NT 16.5
 ACGCTGGTGGTGTGTCACCGGGCGGGCGCGGCTGGACGTGCGC
 Ex 3
 GATGCCTGGGGCCGTCTGCCCCGTGGACCTGGCTGAGGAGCTGGGC
 CATCGCGATGTCGCACGGTACCTGCGCGCGGCTGCGGGGGGCACC
 15
 J(2)
 AGAGGCAGTAACCATGCCCGCATAGATGCCGCGGAAGGTCCCTC
 J(2) Ex 8 Ex 4
 AGACATCCCCGATTGAAAGAACCAGAGAGGCTCTGAGAAACCTC
 Ex 5
 GGGAAACTTAGATCATCAGTCACCGAAGGTCTACAGGGCCACA
 ACTGCCCCCGCCACAACCCACCCCGCTTCGCTAGTTTTTCATTTAGA
 AAATAGAGCTTTTAAAAATGTCCTGCCTTTTAACGTAGATATAA
 GCCTTCCCCCACTACCGTAAATGTCCATTATATCATTTTTTATAT

Figure 1A

ATTCTTATAAAAATGTAAAAAAGAAAAACACCGCTTCTGCCTTT

TCAGTGTGTTGGAGTTTTCTGGAGTGAGCACTCACGCCCTAAGCG

CACATTCATGTGGGCATTTCTTGCGAGCCTCGCAGCCTCCGGAAG

CTGTCGACITCATGACAAGCATTTGTGAACTAGGGAAGCTCAG

GGGGGTTACTGGCTTCTCTTGAGTCACACTGCTAGCAAATGGCAG

AACCAAAGCTCAAATAAAAAATAAAATTATTTTCATTCATTCACT

CAAAAAAA

Figure 1B

Figure 2A

p16EX1 < GGNGGNAAGNTGTGGGGGAAAAGTTTGGGGATGGAANACCAANCCCTCCTTTTCNTTACCAA 60
.....+.....+.....+.....+.....+.....+.....+.....+.....+
p16EX1 < ACNCTGGCTCTGNCGAGGCTNCNTCCGANTGGTNCCCCCGGGGGAGACCCAACCTGGGGNC 120
.....+.....+.....+.....+.....+.....+.....+.....+.....+
p16EX1 < GACTTCAGGGNTGCNACATTCACTAAGTGCTNGGAGNTAATANCACCTCCTCCGAGCANx 180
p16EX13 < TCNCTTATTGNTAGGANATAATAAACACCTCCACCGATAACT 41
.....+.....+.....+.....+.....+.....+.....+.....+.....+
p16EX1 < TCGCTCACAGCGTCCCCTTACCTNGANAGATACCNCgXGxTCCCTCCAGAGGATTTGAGG 240
p16EX13 < TcaCTTACAACGTCCCNNTtCCTGgaAAGATACacaGCGTTCCTCCAGAGGATTTGTGG 101
.....+.....+.....+.....+.....+.....+.....+.....+.....+
p16EX1 < GACAGGNTCGGAGGGGGCTCTTCCCCCANCACCGGAGGAAGAAAGAGGAGGGNCTGACTG 300
p16EX13 < GACAGGGTNGGAGNGGTCTCTTCNCCACCACCGGAGGAAGAAAGAGGAGGGGGCTGNCTG 161
.....+.....+.....+.....+.....+.....+.....+.....+.....+
p16EX1 < GTCACCAGAGGGTGGGACGGACCGCGTGCGCTCGGCGNCTNCGGAGAGGGGGAGAACAGA 360
p16EX13 < TTCACCAGAGGGTGGGACGGACCNCGTACGCTCGNCGNCTNCGGAGAGGGGGAGAGCAGT 221
.....+.....+.....+.....+.....+.....+.....+.....+.....+
p16EX1 < CAACGGGCGGGCGGGGAGCAGCATGGATCCGGCGGCGGGGAGCAGCATGGANCCTTCGACT 420
p16EX13 < CANGGNCGNCGGGGAGCAACATGGAACGNCGGCGGGGAGCAGCATGGANCCTTCGGCT 281
.....+.....+.....+.....+.....+.....+.....+.....+.....+
P16NT2 7 < GACNNNCTCCGGCCGGNGTCCGGGTAGAGGAGGTGCGGGCGCTGCTGGAG 49
p16EX1 < GACTGACTGCCTCGC 435
p16EX13 < GACTGGCTGNCCACGNCCACGNCCCGGGGTCCGGGTAGAGGAGGTGCGGNCGCTNCTGGAG 341
.....+.....+.....+.....+.....+.....+.....+.....+.....+
P16NT3 > GCGGGGGCGCTGCCCAACGCACCGAATAGTTACGGTCCGAGGCCGATCAGGTxxGGGTA 15
P16NT2 < GCGGGGNCCTCTGNCCAACNCGCTAAAAAN 109
p16EX13 < GCGGGGNCCTCTGNCCAACNCGCTAAAAAN 369
.....+.....+.....+.....+.....+.....+.....+.....+.....+
P16NT3 > GAGGGTCTGCAGCGGGAGCAGNGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG 75
P16NT2 < GAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGACTCTGGAGGACGAAGTTTGCAGGGG 169
.....+.....+.....+.....+.....+.....+.....+.....+.....+
P16NT3 > AATTGGAATCAGGTAGCGCTTCGANTCTCCGGAAAAAGGGGAGGCTTCCTGGGGAGTTNN 135
P16NT2 < AATTGGAATCAGGTAGCGCTTCGATTCTCCNGAAAAAGGGGAGGCTTCCTGGGGAGTTT 229

Figure 2B

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.....+.+.+.+.+.+.+.+.+.+.
> CAGAAGGGGTTTGTAAATCACAGNCCTCCNCCTGGCGACGCCCTGGGGGGTTGGGAAGCCA 195
< CAGAAGGGGTTTGTAAATCACAGACCTCCTCCTGGCGACGTCCTGGGGGGCTTGGGAAGCCA 289

.....+.+.+.+.+.+.+.+.+.+.
> AGGAAGAGGAATGAGGAGNCACGCGCNTACAGNTCTCTCGAATNCTGANAAGATCTGAAG 255
< AGGAAGAGGAATNAGGAGCCACGCGCGTACAGATCTCTCGAATGCTGAGAAGATCTNAAG 349

.....+.+.+.+.+.+.+.+.+.+.
> GGGGGAACATATTTGTATTAGxATNNAAGTATGCTCTTTATCAGATACAAAATTCACGAA 315
< GGGGGAACATATTTGTATTAGCNTCCAAGTNTNCTCTNTATCANATACAAANTxC 404

.....+.+.+.+.+.+.+.+.+.+.
> CGTGTGGNATAAAAAGGGAGTCTTAAAGAAATNTAAGATGTGCTGGGACTACTTAGCCTC 375

.....+.+.+.+.+.+.+.+.+.+.
> CAANACACAGATNCCTGGATGGAGCT 401

.....+.+.+.+.+.+.+.+.+.+.

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09016869.013098

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16INT > AAAANNAAAAAAAAAATCTCCCAGGCCTAACATAATTNTCAGGAAAGAAATTTTCAGTAGTTG 60
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
16INT > NATCTCAGGGGAAATACAGGAAGTTAGCCTGGAGTAAAAGTCAGTCTGTCCCTGCCCTT 120
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6INT > TGCTANATTGCCCGTGCTCACAGTGCTCTCTGCCTGTGACGACAGCTCCNCAGAAGTTC 180
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6INT > GGAGGATATAATGGAATTCATTGTGTACTGAAGAATGGATAGAGAACTCAAGAAGGAAAT 240
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6INT > TGGAAACTGGAAGCAAATGTAGGGTAATTAGACACCTGGGGCTTGTGTGGGGGTCTGCT 300
6EX15 < AANAAAAaAgAAATNgAtAANATagAGGAaT 31
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6INT > TGGCGGTGAGGGGGCTCTACACAAGCTTCCTTTCCGTCATGCCGNCCCCACCCTGGCTC 360
6EX15 < GAGCANATTAAAAcAAAAAAGANAAGANagacaTaATAAAAAAcGagATgTTeTAGAS 91
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6INT > TGACCATTCTGTTTCTCTCTGGCAGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTG 420
6EX15 < NTAATcATAATTATAaaaggTeaaagacTcATTGATATnaAGGAaattgaAGGCAATetTa 151
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6INT > CTGCTGCTCCACGGCGCGGAGCCCCAACTGCTCCGACGCCG 460
6EX2 > CCTGCNACGACCCCGCCACTCTCACCCGACCCGTG 35
6EX14 > NCTCTCACGGTGGGGAGGCCAACTGCGCCGAACCCGCCACTCTCACCCGACCCGCG 56
6EX15 < acTagCACANNNGNATNAAAAANAATTccacGACACCGCCACTCTCAACCGATCCGTG 211
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6EX2 > CACGACGCTGTCCGGGAGGGTTTTCTGGACACGCTGGTGGTGTCTGCACCGGGCCGGGGNG 95
6EX14 > CACGACGGTGCCCGGGAGGGGTTTTCTGGACACGCTGGTGGTGTCTGCACCGGGCCGGGGCG 116
6EX15 < CTCGACACTGCCCGGGAGGTCNTCCTGGACACGCTGGTGGTNCTCCACCGGNCCGGGGCA 271
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
6EX2 > CGGTTGGACGTGCGCGATGCCTGGGGCCGCTNCCCGTGGxACCTGGTTGAGGAGCTGGG 155
EX14 > CGGCTGGACGTTTCGNGATGCCTGGGGGCNTCTNTCCGTNGxACCTGGCTGAAGAGCTGGN 176
EX15 < CGTCTGGACGTGCGCGATGCCTGGGNCCGNCTACCCGTGGTACCTGACTGAGGACCTGGG 331
.....+.+.....+.+.....+.+.....+.+.....+.+.....+.+
EX2 > NCATCGCGATGTGCGACGSTACCTGCGCGCGGTTGCGGGGGGGCACCAGAGGxNAGTNACC 215
EX14 > NCATCGNGATGTGCGACGGCCNCTGTGTGNGGNTGCGGGGGGGCACCATAGGTCAGTNTCC 236
EX15 < CCATCCCGATTTCGCGNGGGTANCTGNGNGNGGGCTGNGGGGGGCCAANAGAGGxCANTACCC 391

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016EX5 < XAAGTATGAGCGAAACNAATTGTGGTTTGAGAANAGGNAATCGTAGGGAACTTCGGGGATC 60
+.....+.....+.....+.....+.....+.....+
 016EX5 < CCNCNGGGANCNCCAGAACCTGAGNCGCCNATTGGAAATNACAAACTGNCTGNATCACTC 120
+.....+.....+.....+.....+.....+.....+
 016EX5 < CGNACCAGGTNCAAAAGATACCTGGGGANGCGGGAAGGGAAAGACNACATCNAGACCGCC 180
 016EX9 < CCCC 4
+.....+.....+.....+.....+.....+.....+
 016EX5 < TTCGCNCCTXGGNATTGTGAGCAGCCTCTGAGACTCATTXATATNACACTCGTXXTTTCTT 240
 016EX9 < ATCGCGCCTTGGGANTGTGAGCNACCATTGAGACTCATNAATATAGCACTCGTTTTTCTT 64
+.....+.....+.....+.....+.....+.....+
 016EX5 < CTTACAACCCTGCGGNCCGCGCGGTGCGCCTTTCTCTGCCCTCCGCCGGGTGGACCTGGA 300
 016EX9 < CTTGCAACCCTGCGGNCCGCGCGGTGCGCCTNTCTCTGCCCTCCGCNGGGTGGACCTGGA 124
+.....+.....+.....+.....+.....+.....+
 016EX5 < GCGCTTGAGCGGTTCGGCGCGCCTGGAGCAGCCAGGCGGNCAGTGGACTAGCTGCTGGACC 360
 016EX9 < GCGCTTGAGCGGTTCGGCGCNCCTGGANCAGCCAGGCGGGCAGTGGACTACCTNCTGGACC 184
+.....+.....+.....+.....+.....+.....+
 016EX5 < AGGGAGGTGTGGGAGAGCGGTGGCGGCGGGTACATGCACGTGAAGCCATTGCGAGAACTT 420
 016EX9 < AGGGAGGTGTGGGAGAGCGGTGNCGGCGGGTACATGCACGTGAAGCCATTGCGAGAACTT 244
+.....+.....+.....+.....+.....+.....+
 016EX5 < TATCCATAAGTATTTCAATACCGGTAGGGACGGCAAGAGAGGAGGGCGGGATGTGCCACA 480
 016EX9 < TATCCATAAGTATTTCAATGCCGGTAGGGACGGCAAGAGAGGAGGGCGGGATGTNCCACA 304
+.....+.....+.....+.....+.....+.....+
 016EX5 < CATCTTTGACCTCAGGTTTCTAACGCCTGTTTTCTTTCTGCCCTCTGCAGACAACCCCGA 540
 016EX9 < CATCTTTGACCTCAGGTTTCTAACGCCTGTTTTCTTTCTGCCCTCTGCAGACATCCCGA 364
+.....+.....+.....+.....+.....+.....+
 016EX4 > AGAAATTAGATCATCAGTCACCGATG 26
 016EX5 < TTGAAAGAACCAGAGAGGCTCTGAGAAACC 570
 016EX9 < TTGAAAGAACCAGAGAGGCTCTGAGAAACCTCCGGAAACTTAGxTCATCAxTCGCCGNAA 424
+.....+.....+.....+.....+.....+.....+
 016EX4 > GTCCTACAGGGNCACAACTGNCCCCGCCACAACCCACCCCGNTTTCGTAGTTTTTCATTTA 86
 016EX9 < AA 426
+.....+.....+.....+.....+.....+.....+



6E
6E
6E
6E
6E
6E
6E

Figure 3C

16EX6a > GNGGATTGGNCCACTACGCNTANCCATCACCCCTATTC 515

.....+.....+.....+.....+.....+.....+

09016869 013098

Figure 5

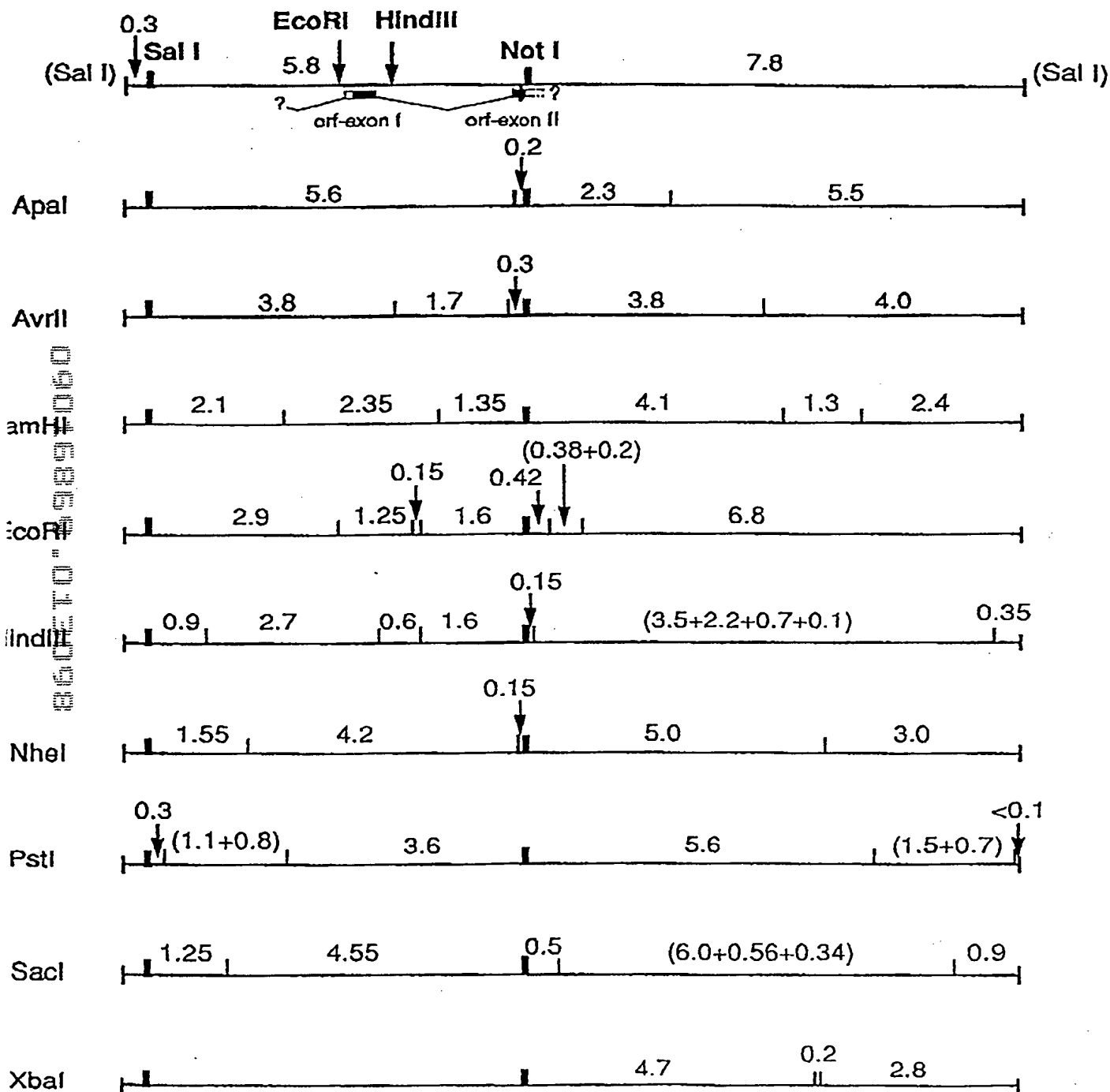


Figure 6

p16: Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala
p15: Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala
p13: Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp Pro *

Thr Leu * Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
Thr Leu * Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg
Thr Thr phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg

Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Leu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg

Ala Ala Ala Gly Gly Thr
Thr Ala Thr Gly Asp
Ser Ala * Gly Cys Ser